

Figure 1A

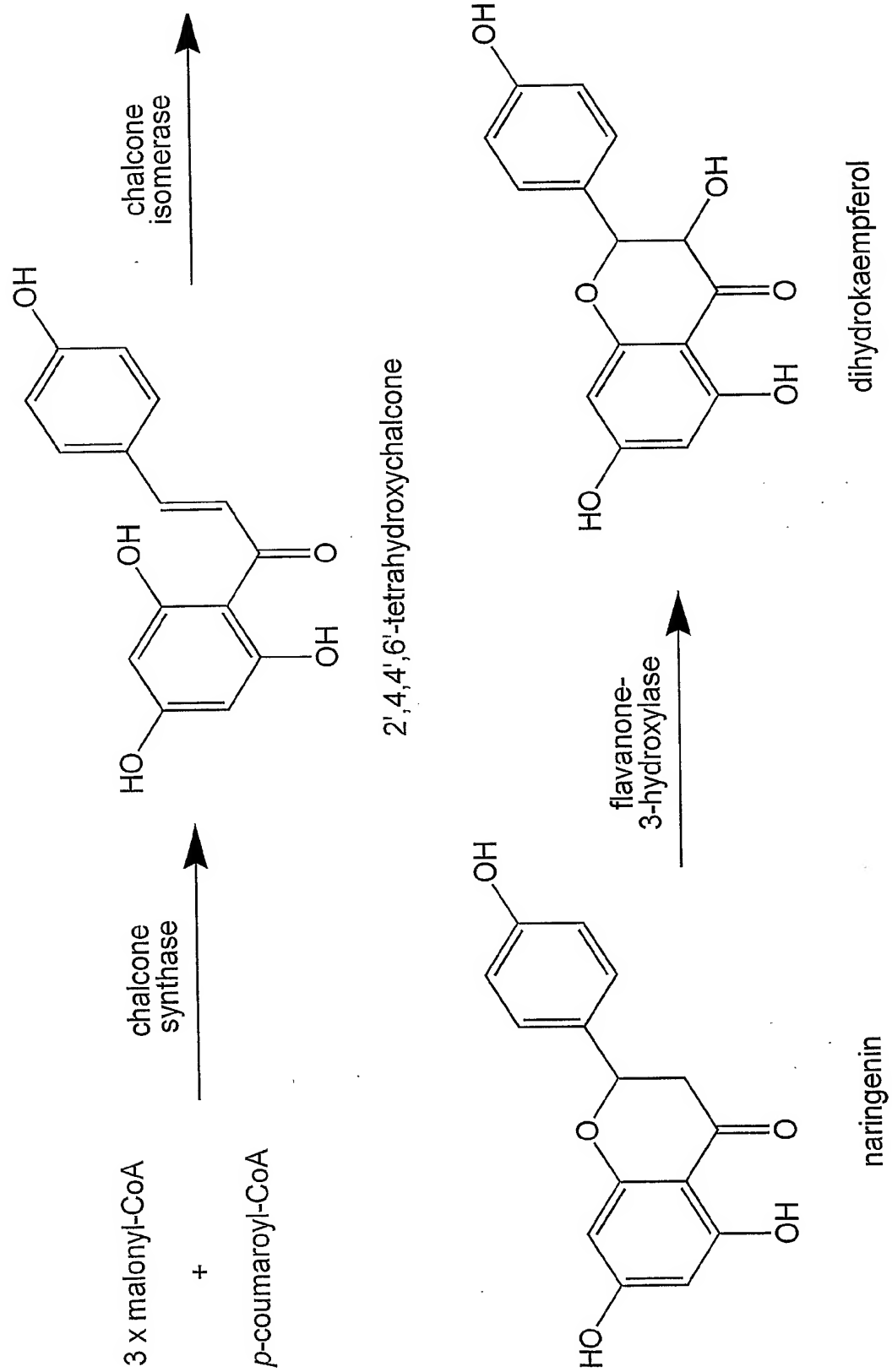


Figure 1B

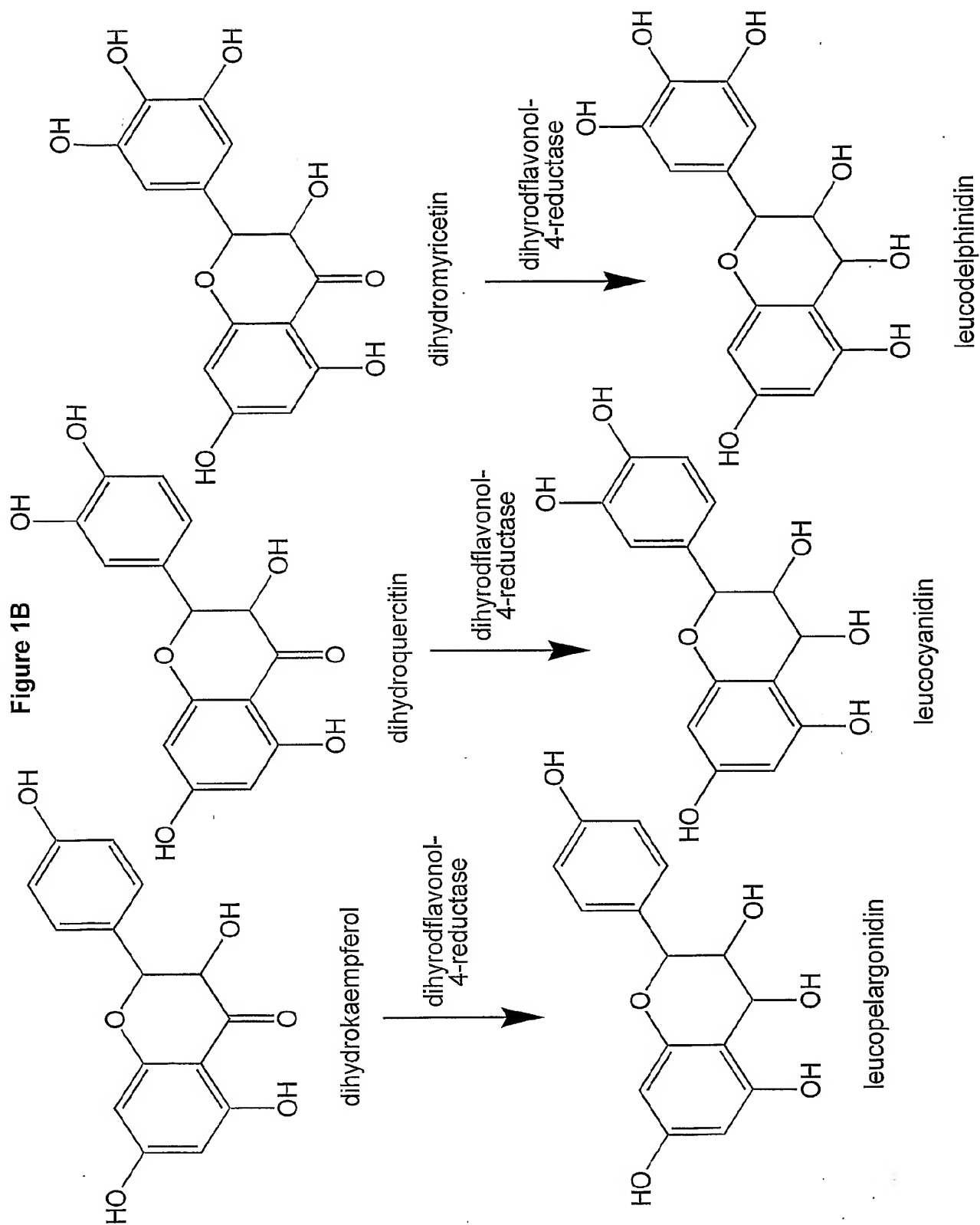


Figure 2A

SEQ ID NO:4	MGSK-----SETVCVTGASGYIGSWLVMRLIERGYTVRATVLDPADMREVKHLLDLP	GAE	55
SEQ ID NO:6	MGSK-----SETVCVTGASGYIGSWLVMRLIERGYTVRATVLDPADMREVKHLLDLP	GAE	55
SEQ ID NO:8	L-----		1
SEQ ID NO:17	MGSA-----SESVCVTGASGFIGSWLVMRLIERGYTVRATVRDPVNMKKVKHVL	PGAK	55
SEQ ID NO:18	MDQTLTHTGSKKACVIGGTGNLASILIKHLLQSGYKVNTTVRDPENEKKIAHLRQLQEL-		59
SEQ ID NO:4	SKLSLWKAELTEEGSFDEAIKGTGVFHLATPVDFEKS	KDPENEMIKPTIQGV	115
SEQ ID NO:6	SKLSLWKAELTEEGSFDEAIKGTGVFHLATPVDFEKS	KDPENEMIKPTIQGV	115
SEQ ID NO:8	-----VFQLATPVNFASEDPENDMIKPAITGV	LVNLKACV	36
SEQ ID NO:17	SKLSLWKADLAEEGSFDEAIKGTGVFHVATPMD	EFESKDPENEVIKPTINGV	115
SEQ ID NO:18	GDLKIFKADLTDEDSFESSFGCEYIFHVATPINF	KSEDPKDMIKPAIQGV	119
SEQ ID NO:4	KAKTVRRLLVFTSSAGTNNITEHQKP--IIDETCWT	DVEFCRRLLNMTGWMYFVSK	173
SEQ ID NO:6	KAKTVRRLLVFTSSAGTNNITEHQKP--IIDETCWT	DVEFCRRLLNMTGWMYFVSK	173
SEQ ID NO:8	RAKGVKRVILTSSAAAVTINQLKGTDLVMD	ESNWTDDVEYLS	96
SEQ ID NO:17	KAKTVRRLLVFTSSAGTLNVIERQKP--VFDDTCW	SDVEFCRRVKMTGWMYFVSK	173
SEQ ID NO:18	KSKSVKRVITYTSSAAAVSINNLSGTGLVMNEENW	TDIDFELTEKPFNWGYPISKV	179



Figure 2C

SEQ ID NO: 4	--	339
SEQ ID NO: 6	--	339
SEQ ID NO: 8	HK	256
SEQ ID NO: 17	HK	347
SEQ ID NO: 18	ES	342

Figure 3A

SEQ ID NO:12	M-DGNKGPVVVTGASGFVGSWLVKLLQVGYTVRATVRDPANVEKNKPLLELPGAKERLS	59
SEQ ID NO:14	MANTSGKGVCTGASGFVASWLVKRLLESGYHVLGTVRDPGNQKKVAHLWNLAGAKEGLE	60
SEQ ID NO:16	M-DGSKGPVVVTGASGFVGSWLVKLLQAGYTVRATVRDPANVEKNKPLLELPGAKERLS	59
SEQ ID NO:19	M-DGNKGPVVVTGASGFVGSWLVKLLQAGYTVRATVRDPANVEKTKPLLELPGAKERLS	59
SEQ ID NO:20	MVISSKGVCTGASGFVASWLVKRLLEAGYHVIGTVRDPNREKVSHLWRLPSAKERLQ	60
SEQ ID NO:12	IWKADLSEEGSFDDAIAAGCTGVFHVATPMDFDSDQP-ENEVIKPTVEGMLSIMRACKEAG	118
SEQ ID NO:14	LVRADLLEEGSFDDAVMACEGVFHTASPIITNADS--KEEMLD SAINGTLNVLRSCKKNP	118
SEQ ID NO:16	IWKADLSDEGSFDDAIAAGCTGVFHVATPMDFDSDKP-ENEVIKPTVEGMLSIMRACKEAG	118
SEQ ID NO:19	IWKADLSEDSFNEAIAAGCTGVFHVATPMDFDSDQP-ENEVIKPTVEGMLSIMRACKEAG	118
SEQ ID NO:20	LVRADLMEEGSFDDAVMACEGVFHTASPVLA KSDSNCKEMLVPAINGTLNVLKSCCKNP	120
SEQ ID NO:12	TVKRIVFTSSAGSVNIEE---RQRPAYDQDNWSDIDFCRRVKMTGWMYFVSKSLAEKAA	174
SEQ ID NO:14	FLKRIVLTSSSSTMRRLRDEAEFFPPNVLLDETSSWSSVEFCESIQI--W-YAVAKILAEKSA	175
SEQ ID NO:16	TVKRIVFTSSAGSVNIEE---RQRPAYDQDNWSDIDFCRRVKMTGWMYFVSKSLAEKAA	174
SEQ ID NO:19	TVKRIVFTSSAGSVNIEE---RPRPAYDQDNWSDIDYCRRVKMTGWMYFVSKALAEKAA	174
SEQ ID NO:20	FLKRIVLTSSSSTVRIMDESK-HPEISLDETIWSSVALCEKLQ--W-YALAKISAEKAA	176

Figure 3B

SEQ ID NO:12	190	200	210	220	230	240	234
SEQ ID NO:14	MEYASENGLDFISIIPTLVVGPFLSAGMPPSLV	TALALITGNEAHYSILKQVQVLVHLDDL					235
SEQ ID NO:16	WEFAKENNIDLVAVLPTFIIGPNLSPVLGPTASD	VLGLFKGETEKFTIFGRMGYVHIDDV					234
SEQ ID NO:19	MEYASENGLDFISIIPTLVVGPFLSAGMPPSLV	TALALITGNEAHYSILKQVQVLVHLDDL					234
SEQ ID NO:20	MEYASENGLDFISIIPTLVVGPFLSAGMPPSLV	TALALITGNEAHYSILKQVQVLVHLDDL					236
	WEFAKENNIDLVTPLPSFVIGPSLSHEL	SVTASDIILGLIQGDTDRFISYGRMGYVHIDDV					
SEQ ID NO:12	250	260	270	280	290	300	294
SEQ ID NO:14	CDAMTFLFEHPEANGRYICSSHDATIHGLARMLR	DRFPEYSIPQKFAGVDDDLQPIHFSS					294
SEQ ID NO:16	ASCHILVYETADAKGRYICNSAVLDSNELVALLA	KREFSFPIPKSLPNYGE-QTYGYNT					294
SEQ ID NO:19	CDAMTFLFEHPEANGRYICSSHDATIHGLARMLR	DRFPEYSIPHKFAGVDDDLQPIHFSS					294
SEQ ID NO:20	CDAMTFLFEHPEANGRYICSSHDATIHGLARMLQ	DRFPEYDIPQKFAGVDDNLQPIHFSS					295
	ASCHILVYEAPQATGRYLCNSVVLDNNELVALLA	KQFPIFPIPRSLRNPYEK-QSYELNT					
SEQ ID NO:12	310	320	330	340	350	360	354
SEQ ID NO:14	KKLLDHGFSFRYTAEDMFDAAI	RTCREKGLIPLGDAPPPAAGGKL	GALAAAGEGQAIGAET				329
SEQ ID NO:16	SKIRKLGLEFR-GVEEMFDDSVESLKAHGYL						354
SEQ ID NO:19	KKLLDHGFSFRYTAEDMFDAAI	RTCREKGLIPLGDAPAPAAAGKL	GALAAAGKQAIGAET				354
SEQ ID NO:20	KKLLDHGFSFRYTTEDMFDAAI	HTCRDKGLIPLGDVPAPAAAGKL	GALAAAGEGQAIGAET				330
	SKIQQLGFKFK-GVQEMFGDCVESLKDQGH						